

1 ATGATTACAATAGTTTATTAATCCTAGCCTATCTGCTGGGTTCCATTCTGGTCTGGATTGGACAAGTATCTTTCAAATCAATCTACGGAGC 100
TACTAATGTTATCAAAATATTAGGATCGGATAGACGACCAAGCTAAGGTAGACCAGAGACCTAACCTGTTTATAAGAAAGTTTAGTTAGATCGGCTCG

1 M I T I V L L I L A Y L L G S I P S G L W I G Q V F F Q I N L R E H 34

101 ATGGTCTGGTAAACACTGGAACGACCAACACCTTCGGCATTTTAGGTAAGAAAGCTGGTATGGCAACCTTTGTGATTGACTTTTTCAAAGGAACCCCTAGC 200
TACCAAGACCATTGTGACCTTGCTGGTTGTGAAGGCGTAAATCCATTCTTTCCACCATACCGTTGGAAACACTAACTGAAATAAGTTTCTCTGGGATCG

35 G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A 67

201 AACGCTGCTTCGGATTATTTTTCATCTACAAGGCGTTTCTCCTCTCATCTTTGGACTTTTGGCTGTTATCGGCCATACCTTCCCTATCTTTGCAGGATTT 300
TTGGACGAAAGGCTAATAAAAAAGTAGATGTTCCGCAAGAGGAGAGTAGAATCCTGAAACCGACAATAGCCGGTATGGAAGGATAGAAACGTCCTAA

68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100

301 AAAGGTGGTAAGGCTGTCCCAACCAAGTCTGGAGTGATTTTCGGATTTCGGCTATCTTCTGTCTACCTTGGCTATCTTCTTTGGAGCTCTCTATC 400
TTTCCACCATTCCGACAGCGTTGGTCACGACCTCACTAAAAGCTAAACGGGATAGAACGAGATGGAACGCTAATAGAAACCTCGAGAGATAG

101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134

401 TTGGCAGTATGATTTCACTGTCTAGTGTACAGCATCGATTGGCGCTGTTATCGGGTTCTGCTCTTCCACTTTTGGTTTATCCTGAGTAACATGA 500
AACCGTCATACTAAAGTGACAGATCACAGTGTGCTAGCTAACCGCGACAATAGCCCAAGACGAGAAAGGTGAAACCAAAATAGGACTCATTTGATCT

135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167

501 CTCTCTTTCATCGCTATTATCTTAGCACTTGTAGTTTATCATTCGTCAAGGACAAATATAGCTCGTATCAAAATAAACTGAAATTTGGTC 600
GAGAGAGAGTAGCGATAATAGATCGTGAACGATCAAACTAATAGTAGCAGTATTCCTGTTATATCGAGCATAGTTTATTTTGTACTTTTAAACCAG

168 S L F I A I I L A L A S L I I I R H K D N I A R I K N K T E N L V 200

601 CCTTGGGGATTGAACCTAACCCATCAAGATCCTAAAAATAA 642 SEQ ID NO:2
GGAACCCCTAACTGGATTGGGTAGTCTAGGATTTTATT SEQ ID NO:11

201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

FIG. 1

1 ATGATTACAATAGTTTATTAATCCTAGCCTATCTGCTGGGTTGCAATCTGGTCTCTGGATTGGACAAGTATTCTTCAAATCAATCTACGCGAGC 100
TACTAATGTTATCAANAATAATTAGGATCGGATAGACGACCAAGCTAAGGTAGACCAGAGACCTAACCTGTTTCATAAGAAAAGTTTAGTTAGATGCGCTCG

1 M I T I V L L I L A Y L L G S I P S G L W I G Q V F F Q I N L R E H 34

101 ATGGTTCTGGTAACACTGGAAACGACCAACCTTCCGCAATTTTAGGTAAAGAAAGCTGGTATGGCAACCTTTGTGATTGACTTTTCAAAGGAACCCCTAGC 200
TACCAAGACCAATTGTGACCTTGTGCTGTTGTGGAAGGCGTAAATCCATTTCTTCGACCATAACCGTTGGAAACACTAACTGAAGAAAGTTTCTTGGGATCG

35 G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A 67

201 AACGCTGCTCCGATTATTTTTCATCTACAAGGCGTTTCTCCTCTCATCTTTGGACTTTTGGCTGTTATCGGCCATACCTTCCCTATCTTTGCGAGGATTT 300
TTGCGACGAAGGCTAATAAAGTAGATGTTCCGCAAGAGGAGAGTAGAAACCTGAAACCGACAAATAGCCGGTATGGAAAGGATAGAAACGTCCTCTAAA

68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100

301 AAAGGTGGTAAGGCTGTCCCAACCAAGTCTGGAGTGATTTTCGGATTGCGCCTATCTTCTGCTCTACCTTGGGATTATCTTCTTTGGAGCTCTCTATC 400
TTTCCACCAATCCGACAGCGTTGGTCACGACCTCACTAAAGCCTAAACCGCGATAGAAAGACAGAGATGGAAACGCTAATAGAAAGAAACCTCGAGAGATAG

101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134

401 TTGGCAGTATGATTTCACTGTCTAGTGTACAGCATCGATTGGGCTGTTATCGGGGTTCTGCTCTTTCCACTTTTGGTGTATCTCTGAGTAACCTATGA 500
AACCCTCATACTAAAGTGACAGATCACAGTGTCTAGCTAACGCCGACAAATAGCCCCAAGACGAGAAAGGTGAAGAAACCAAAATAGGACTCATTTGATACT

135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167

501 CTCTCTCTTCATCGCTATTATCTTAGCACTTGTCTAGTTTGATTATCATTTGTCATAGGACAAATAGCTCGTATCAAAATAAACTGAAGAAATTTGGTC 600
GAGAGAGAAAGTAGCGATAATAGATCGTGAACGATCAAACTAATAGTAAGCAGTATTCCTGTATATCGAGCATAGTTTATTTTGACTTTTAAACCCAG

168 S L F I A I I L A L A S L I I I R H K D N I A R I K N K T E N L V 200

601 CCTTGGGGATTGAACCTAACCCATCAAGATCCTAAATAAATAA 642 SEQ ID NO:2
GGAAACCCCTAACTTGGATTGGGTAGTTCTAGGATTTTATTT 643 SEQ ID NO:11

201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

FIG. 1